

AMENDMENTS TO THE CLAIMS:

The following is the status of the claims of the above-captioned application, as amended.

Claims 1-57 (Canceled)

Claim 58 (Currently amended). ~~A-An isolated mutated prokaryotic Bacillus cell, which has a reduced expression-level of polypeptide having at least 90% sequence identity to YusZ (SEQ ID NO's: 2 or 25), YusX (SEQ ID NO: 4) or YusY (SEQ ID NO: 5), or homologues thereof, and which secretes higher amounts of at least one heterologous polypeptide of interest, when compared with an otherwise isogenic but non-mutated cell.~~

Claims 59-60 (Canceled).

Claim 61 (Previously presented). The cell of claim 60, which is a *B.alkalophilus*, *B.amylolyticus*, *B.brevis*, *B.circulans*, *B.clausii*, *B.coagulans*, *B.lautus*, *B.lentus*, *B/licheniformis*, *B.megaterium*, *B.stearothermophilus*, *B.subtilis*, or *B.thuringiensis* cell.

Claim 62 (Currently amended). The cell of claim 58, wherein ~~the polypeptide has at least 95% sequence identity to the polypeptide of SEQ ID NO: 2, SEQ ID NO: 25 or SEQ ID NO: 4, or YusZ or YusX homologues comprise an amino acid sequence at least 70% identical to the sequence shown in SEQ ID NO's: 2 or 25; or SEQ ID NO: 4, respectively.~~

Claim 63 (Currently amended). The cell of claim 58, which is mutated in *yusZ* (~~SEQ ID NO's: 1 or 24~~), *yusX* (~~SEQ ID NO: 3~~), and/or *yusY* (~~SEQ ID NO: 5~~), or homologues thereof, wherein the polypeptide has at least 97% sequence identity to the polypeptide of SEQ ID NO: 2, SEQ ID NO: 25 or SEQ ID NO: 4.

Claim 64 (Currently amended). The cell of claim 63, wherein ~~the polypeptide has at least 99% sequence identity to the mature polypeptide of SEQ ID NO: 2, SEQ ID NO: 25 or SEQ ID NO: 4~~.
~~the yusZ, yusX, and/or yusY homologues encode a polypeptide having an amino acid sequence at least 70% identical to the sequence shown in SEQ ID NO's: 2 or 25, SEQ ID NO: 4, or SEQ ID NO: 6, respectively.~~

Claim 65 (Currently amended). The cell of claim 63, wherein

the polypeptide comprises the polypeptide of SEQ ID NO: 2, SEQ ID NO: 25 or SEQ ID NO: 4.
~~the yusZ, yusX, and/or yusY homologues have a nucleotide sequence at least 70% identical to the sequence shown in SEQ ID NO's: 1 or 24, SEQ ID NO: 3, or SEQ ID NO: 5, respectively.~~

Claim 66 (Previously presented). The cell of claim 58, which is mutated in at least one polynucleotide, where a subsequence having a size of at least 100 bp of the at least one polynucleotide hybridizes with a polynucleotide having the sequence shown in SEQ ID NO's: 1 or 24, SEQ ID NO: 3, or SEQ ID NO: 5, or the respective complementary sequences, under medium stringency hybridization conditions.

Claim 67 (Previously presented). The cell of claim 58, wherein the at least one heterologous polypeptide comprises an enzyme.

Claim 68 (Currently amended). A method for producing a polypeptide of interest, said method comprising the steps of:

- a) cultivating a mutated prokaryotic Bacillus cell, which has a reduced expression-level of polypeptide having at least 90% sequence identity to the polypeptide of SEQ ID NO: 2, SEQ ID NO: 25 or SEQ ID NO: 4, YusZ (SEQ ID NO's: 2 or 25), YusX (SEQ ID NO: 4), or homologues thereof, and which secretes higher amounts of the polypeptide of interest, when compared with an otherwise isogenic but non-mutated cell; and
- b) isolating the polypeptide of interest.

Claim 69-70 (Canceled).

Claim 71 (Previously presented). The method of claim 70, wherein the cell is a *B.alkalophilus*, *B.amylolyquefaciens*, *B.brevis*, *B.circulans*, *B.clausii*, *B.coagulans*, *B.lautus*, *B.lentus*, *B/licheniformis*, *B.megaterium*, *B.stearothermophilus*, *B.subtilis*, or *B.thuringiensis* cell.

Claim 72 (Currently amended). The method of claim 68, wherein the polypeptide has at least 95% sequence identity to the polypeptide of SEQ ID NO: 2, SEQ ID NO: 25 or SEQ ID NO: 4, the YusZ or YusX homologues comprise an amino acid sequence at least 70% identical to the sequence shown in SEQ ID NO's: 2 or 25, or SEQ ID NO: 4, respectively.

Claim 73 (Currently amended). The method of claim 68, wherein the cell in step (a) is mutated in a position characterized as within SEQ ID NO: 1, SEQ ID NO: 24 or SEQ ID NO:

~~25 yusZ (SEQ ID NO's: 1 or 24), yusX (SEQ ID NO: 3), and/or yusY (SEQ ID NO: 5), or homologues thereof.~~

Claim 74 (Currently amended). The method of claim 73, wherein ~~the polypeptide has at least 97% sequence identity to the polypeptide of SEQ ID NO: 2, SEQ ID NO: 25 or SEQ ID NO: 4, the yusZ, yusX, and/or yusY homologues encode a polypeptide having an amino acid sequence at least 70% identical to the sequence shown in SEQ ID NO's: 2 or 25, SEQ ID NO: 4, or SEQ ID NO: 6, respectively.~~

Claim 75 (Currently amended). The method of claim 73, wherein ~~the polypeptide has at least 99% sequence identity to the polypeptide of SEQ ID NO: 2, SEQ ID NO: 25 or SEQ ID NO: 4, the yusZ, yusX, and/or yusY homologues have a nucleotide sequence at least 70% identical to the sequence shown in SEQ ID NO's: 1 or 24, SEQ ID NO: 3, or SEQ ID NO: 5, respectively.~~

Claim 76 (Previously presented). The method of claim 68, wherein the cell in step (a) is mutated in at least one polynucleotide, wherein a subsequence having a size of at least 100 bp of the at least one polynucleotide hybridizes with a polynucleotide having the sequence shown in SEQ ID NO's: 1 or 24, SEQ ID NO: 3, or SEQ ID NO: 5, or the respective complementary sequences, under medium stringency hybridization conditions.

Claim 77 (Previously presented). The method of claim 68, wherein the at least one polypeptide of interest comprises an enzyme.